SEQUENCE LISTING

<110> Brzostowicz, Patricia C.
      Cheng, Qiong
      DiCosimo, Deana J.
      Koffas, Mattheos
      Miller, Edward S. Jr.
      Odom, J. Martin
      Picataggio, Steve
      Rouviere, Pierre E.

<120> CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE

<400> 1

```
gatgtggtca catggcccta tcacttaacg gctgatattc gattttgtca ttggtttttt      60

cttaactttta acttctacac gctcatgaac aaacctaaaa aagttgcaat actgacagca     120

ggcggcttgg cgccttgttt gaattccgca atcggtagtt tgatcgaacg ttataccgaa     180

atcgatccta gcatagaaat catttgctat cgcggcggtt ataaaggcct gttgctgggc     240

gattcttatc cagtaacggc cgaagtgcgt aaaaaggcgg gtgttctgca acgttttggc     300

ggttctgtga tcggcaacag ccgcgtcaaa ttgaccaatg tcaaagactg cgtgaaacgc     360

ggtttggtca agagggtga agatccgcaa aaagtcgcgg ctgatcaatt ggttaaggat     420

ggtgtcgata ttctgcacac catcggcggc gatgatacca atacggcagc agcggatttg     480

gcagcattcc tggccagaaa taattacgga ctgaccgtca ttggtttacc taaaaccgtc     540

gataacgacg tatttccgat caagcaatca ctaggtgctt ggactgccgc cgagcaaggc     600

gcgcgttatt tcatgaacgt ggtggccgaa aacaacgcca acccacgcat gctgatcgta     660

cacgaagtga tgggccgtaa ctgcggctgg ctgaccgctg caaccgcgca ggaatatcgc     720
```

```
aaattactgg  accgtgccga  gtggttgccg  gaattgggtt  tgactcgtga  atcttatgaa      780

gtgcacgcgg  tattcgttcc  ggaaatggcg  atcgacctgg  aagccgaagc  caagcgcctg      840

cgcgaagtga  tggacaaagt  cgattgcgtc  aacatcttcg  tttccgaagg  tgccggcgtc      900

gaagctatcg  tcgcggaaat  gcaggccaaa  ggccaggaag  tgccgcgcga  tgcgttcggc      960

cacatcaaac  tggatgcggt  caaccctggt  aaatggttcg  gcgagcaatt  cgcgcagatg     1020

ataggcgcgg  aaaaaaccct  ggtacaaaaa  tcgggatact  tcgcccgtgc  ttctgcttcc     1080

aacgttgacg  acatgcgttt  gatcaaatcg  tgcgccgact  ggcggtcga  gtgcgcgttc      1140

cgccgcgagt  ctggcgtgat  cggtcacgac  gaagacaacg  gcaacgtgtt  gcgtgcgatc     1200

gagtttccgc  gcatcaaggg  cggcaaaccg  ttcaatatcg  acaccgactg  gttcaatagc     1260

atgttgagcg  aaatcggcca  gcctaaaggc  ggtaaagtcg  aagtcagcca  c             1311


<210>  2
<211>  437
<212>  PRT
<213>  Methylomonas 16a

<400>  2

Asp Val Val Thr Trp Pro Tyr His Leu Thr Ala Asp Ile Arg Phe Cys
1               5                   10                  15


His Trp Phe Phe Leu Asn Phe Asn Phe Tyr Thr Leu Met Asn Lys Pro
            20                  25                  30


Lys Lys Val Ala Ile Leu Thr Ala Gly Gly Leu Ala Pro Cys Leu Asn
        35                  40                  45


Ser Ala Ile Gly Ser Leu Ile Glu Arg Tyr Thr Glu Ile Asp Pro Ser
        50                  55                  60


Ile Glu Ile Ile Cys Tyr Arg Gly Gly Tyr Lys Gly Leu Leu Leu Gly
65                  70                  75                  80


Asp Ser Tyr Pro Val Thr Ala Glu Val Arg Lys Lys Ala Gly Val Leu
                85                  90                  95


Gln Arg Phe Gly Gly Ser Val Ile Gly Asn Ser Arg Val Lys Leu Thr
            100                 105                 110


Asn Val Lys Asp Cys Val Lys Arg Gly Leu Val Lys Glu Gly Glu Asp
            115                 120                 125
```

2

Pro Gln Lys Val Ala Ala Asp Gln Leu Val Lys Asp Gly Val Asp Ile
    130   135   140

Leu His Thr Ile Gly Gly Asp Asp Thr Asn Thr Ala Ala Ala Asp Leu
145   150   155   160

Ala Ala Phe Leu Ala Arg Asn Asn Tyr Gly Leu Thr Val Ile Gly Leu
            165   170   175

Pro Lys Thr Val Asp Asn Asp Val Phe Pro Ile Lys Gln Ser Leu Gly
            180   185   190

Ala Trp Thr Ala Ala Glu Gln Gly Ala Arg Tyr Phe Met Asn Val Val
            195   200   205

Ala Glu Asn Asn Ala Asn Pro Arg Met Leu Ile Val His Glu Val Met
    210   215   220

Gly Arg Asn Cys Gly Trp Leu Thr Ala Ala Thr Ala Gln Glu Tyr Arg
225   230   235   240

Lys Leu Leu Asp Arg Ala Glu Trp Leu Pro Glu Leu Gly Leu Thr Arg
            245   250   255

Glu Ser Tyr Glu Val His Ala Val Phe Val Pro Glu Met Ala Ile Asp
            260   265   270

Leu Glu Ala Glu Ala Lys Arg Leu Arg Glu Val Met Asp Lys Val Asp
    275   280   285

Cys Val Asn Ile Phe Val Ser Glu Gly Ala Gly Val Glu Ala Ile Val
    290   295   300

Ala Glu Met Gln Ala Lys Gly Gln Glu Val Pro Arg Asp Ala Phe Gly
305   310   315   320

His Ile Lys Leu Asp Ala Val Asn Pro Gly Lys Trp Phe Gly Glu Gln
            325   330   335

Phe Ala Gln Met Ile Gly Ala Glu Lys Thr Leu Val Gln Lys Ser Gly
            340   345   350

Tyr Phe Ala Arg Ala Ser Ala Ser Asn Val Asp Asp Met Arg Leu Ile
            355   360   365

3

```
Lys Ser Cys Ala Asp Leu Ala Val Glu Cys Ala Phe Arg Arg Glu Ser
    370             375             380

Gly Val Ile Gly His Asp Glu Asp Asn Gly Asn Val Leu Arg Ala Ile
385             390             395             400

Glu Phe Pro Arg Ile Lys Gly Gly Lys Pro Phe Asn Ile Asp Thr Asp
            405             410             415

Trp Phe Asn Ser Met Leu Ser Glu Ile Gly Gln Pro Lys Gly Gly Lys
            420             425             430

Val Glu Val Ser His
        435


<210>  3
<211>  636
<212>  DNA
<213>  Methylomonas 16a

<400>  3
gaaaatacta tgtccgtcac catcaaagaa gtcatgacca cctcgcccgt tatgccggtc      60

atggtcatca atcatctgga acatgccgtc cctctggctc gcgcgctagt cgacggtggc     120

ttgaaagttt tggagatcac attgcgcacg ccggtggcac tggaatgtat ccgacgtatc     180

aaagccgaag taccggacgc catcgtcggc gcgggcacca tcatcaaccc tcataccttg     240

tatcaagcga ttgacgccgg tgcggaattc atcgtcagcc ccggcatcac cgaaaatcta     300

ctcaacgaag cgctagcatc cggcgtgcct atcctgcccg gcgtcatcac acccagcgag     360

gtcatgcgtt tattggaaaa aggcatcaat gcgatgaaat ctttccggc tgaagccgcc      420

ggcggcatac cgatgctgaa atcccttggc ggccccttgc cgcaagtcac cttctgtccg     480

accggcggcg tcaatcccaa aaacgcgccc gaatatctgg cattgaaaaa tgtcgcctgc     540

gtcggcggct cctggatggc gccggccgat ctggtagatg ccgaagactg gcggaaatc     600

acgcggcggg cgagcgaggc cgcggcattg aaaaaa                               636


<210>  4
<211>  212
<212>  PRT
<213>  Methylomonas 16a

<400>  4

Glu Asn Thr Met Ser Val Thr Ile Lys Glu Val Met Thr Thr Ser Pro
1               5               10              15
```

4

```
Val Met Pro Val Met Val Ile Asn His Leu Glu His Ala Val Pro Leu
            20              25              30

Ala Arg Ala Leu Val Asp Gly Gly Leu Lys Val Leu Glu Ile Thr Leu
            35              40              45

Arg Thr Pro Val Ala Leu Glu Cys Ile Arg Arg Ile Lys Ala Glu Val
        50              55              60

Pro Asp Ala Ile Val Gly Ala Gly Thr Ile Ile Asn Pro His Thr Leu
65              70              75              80

Tyr Gln Ala Ile Asp Ala Gly Ala Glu Phe Ile Val Ser Pro Gly Ile
                85              90              95

Thr Glu Asn Leu Leu Asn Glu Ala Leu Ala Ser Gly Val Pro Ile Leu
            100             105             110

Pro Gly Val Ile Thr Pro Ser Glu Val Met Arg Leu Leu Glu Lys Gly
            115             120             125

Ile Asn Ala Met Lys Phe Phe Pro Ala Glu Ala Ala Gly Gly Ile Pro
    130             135             140

Met Leu Lys Ser Leu Gly Gly Pro Leu Pro Gln Val Thr Phe Cys Pro
145             150             155             160

Thr Gly Gly Val Asn Pro Lys Asn Ala Pro Glu Tyr Leu Ala Leu Lys
                165             170             175

Asn Val Ala Cys Val Gly Gly Ser Trp Met Ala Pro Ala Asp Leu Val
            180             185             190

Asp Ala Glu Asp Trp Ala Glu Ile Thr Arg Arg Ala Ser Glu Ala Ala
            195             200             205

Ala Leu Lys Lys
    210


<210>   5
<211>   1860
<212>   DNA
<213>   Methylomonas 16a
```

5

<400> 5

```
atgaaactga ccaccgacta tcccttgctt aaaaacatcc acacgccggc ggacatacgc      60

gcgctgtcca aggaccagct ccagcaactg gctgacgagg tgcgcggcta tctgacccac     120

acggtcagca tttccggcgg ccattttgcg gccggcctcg caccgtgga  actgaccgtg     180

gccttgcatt atgtgttcaa tacccccgtc gatcagttgg tctgggacgt gggccatcag     240

gcctatccgc acaagattct gaccggtcgc aaggagcgca tgccgaccat tcgcaccctg     300

ggcggggtgt cagcctttcc ggcgcgggac gagagcgaat acgatgcctt cggcgtcggc     360

cattccagca cctcgatcag cgcggcactg ggcatggcca ttgcgtcgca gctgcgcggc     420

gaagacaaga agatggtagc catcatcggc gacggttcca tcaccggcgg catggcctat     480

gaggcgatga atcatgccgg cgatgtgaat gccaacctgc tggtgatctt gaacgacaac     540

gatatgtcga tctcgccgcc ggtcggggcg atgaacaatt atctgaccaa ggtgttgtcg     600

agcaagtttt attcgtcggt gcgggaagag agcaagaaag ctctggccaa gatgccgtcg     660

gtgtgggaac tggcgcgcaa gaccgaggaa cacgtgaagg gcatgatcgt gcccggtacc     720

ttgttcgagg aattgggctt caattatttc ggcccgatcg acggccatga tgtcgagatg     780

ctggtgtcga ccctggaaaa tctgaaggat ttgaccgggc cggtattcct gcatgtggtg     840

accaagaagg gcaaaggcta tgcgccagcc gagaagaccc gttggcctta ccatggcgtg     900

ccggctttcg atccgaccaa ggatttcctg cccaaggcgg cgccgtcgcc gcatccgacc     960

tataccgagg tgttcggccg ctggctgtgc gacatggcgg ctcaagacga gcgcttgctg    1020

ggcatcacgc cggcgatgcg cgaaggctct ggtttggtgg aattctcaca gaaatttccg    1080

aatcgctatt tcgatgtcgc catcgccgag cagcatgcgg tgaccttggc cgccggccag    1140

gcctgccagg cgccaagcc ggtggtggcg atttattcca ccttcctgca acgcggttac    1200

gatcagttga tccacgacgt ggccttgcag aacttagata tgctctttgc actggatcgt    1260

gccggcttgg tcggcccgga tggaccgacc catgctggcg cctttgatta cagctacatg    1320

cgctgtattc cgaacatgct gatcatggct ccagccgacg agaacgagtg caggcagatg    1380

ctgaccaccg gcttccaaca ccatggcccg gcttcggtgc gctatccgcg cggcaaaggg    1440

cccggggcgg caatcgatcc gaccctgacc gcgctggaga tcggcaaggc cgaagtcaga    1500

caccacggca gccgcatcgc cattctggcc tggggcagca tggtcacgcc tgccgtcgaa    1560

gccggcaagc agctgggcgc gacggtggtg aacatgcgtt tcgtcaagcc gttcgatcaa    1620

gccttggtgc tggaattggc caggacgcac gatgtgttcg tcaccgtcga ggaaaacgtc    1680

atcgccggcg cgctggcag  tgcgatcaac accttcctgc aggcgcagaa ggtgctgatg    1740
```

6

```
ccggtctgca acatcggcct gcccgaccgc ttcgtcgagc aaggtagtcg cgaggaattg    1800

ctcagcctgg tcggcctcga cagcaagggc atcctcgcca ccatcgaaca gttttgcgct    1860
```

<210> 6
<211> 620
<212> PRT
<213> Methylomonas 16a

<400> 6

```
Met Lys Leu Thr Thr Asp Tyr Pro Leu Leu Lys Asn Ile His Thr Pro
1               5                   10                  15


Ala Asp Ile Arg Ala Leu Ser Lys Asp Gln Leu Gln Gln Leu Ala Asp
            20                  25                  30


Glu Val Arg Gly Tyr Leu Thr His Thr Val Ser Ile Ser Gly Gly His
            35                  40                  45


Phe Ala Ala Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr
    50                  55                  60


Val Phe Asn Thr Pro Val Asp Gln Leu Val Trp Asp Val Gly His Gln
65                  70                  75                  80


Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Lys Glu Arg Met Pro Thr
                85                  90                  95


Ile Arg Thr Leu Gly Gly Val Ser Ala Phe Pro Ala Arg Asp Glu Ser
            100                 105                 110


Glu Tyr Asp Ala Phe Gly Val Gly His Ser Ser Thr Ser Ile Ser Ala
            115                 120                 125


Ala Leu Gly Met Ala Ile Ala Ser Gln Leu Arg Gly Glu Asp Lys Lys
    130                 135                 140


Met Val Ala Ile Ile Gly Asp Gly Ser Ile Thr Gly Gly Met Ala Tyr
145                 150                 155                 160


Glu Ala Met Asn His Ala Gly Asp Val Asn Ala Asn Leu Leu Val Ile
                165                 170                 175


Leu Asn Asp Asn Asp Met Ser Ile Ser Pro Pro Val Gly Ala Met Asn
            180                 185                 190
```

7

```
Asn Tyr Leu Thr Lys Val Leu Ser Ser Lys Phe Tyr Ser Ser Val Arg
        195             200             205

Glu Glu Ser Lys Lys Ala Leu Ala Lys Met Pro Ser Val Trp Glu Leu
        210             215             220

Ala Arg Lys Thr Glu Glu His Val Lys Gly Met Ile Val Pro Gly Thr
225             230             235             240

Leu Phe Glu Glu Leu Gly Phe Asn Tyr Phe Gly Pro Ile Asp Gly His
            245             250             255

Asp Val Glu Met Leu Val Ser Thr Leu Glu Asn Leu Lys Asp Leu Thr
            260             265             270

Gly Pro Val Phe Leu His Val Val Thr Lys Lys Gly Lys Gly Tyr Ala
            275             280             285

Pro Ala Glu Lys Asp Pro Leu Ala Tyr His Gly Val Pro Ala Phe Asp
        290             295             300

Pro Thr Lys Asp Phe Leu Pro Lys Ala Ala Pro Ser Pro His Pro Thr
305             310             315             320

Tyr Thr Glu Val Phe Gly Arg Trp Leu Cys Asp Met Ala Ala Gln Asp
            325             330             335

Glu Arg Leu Leu Gly Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Leu
            340             345             350

Val Glu Phe Ser Gln Lys Phe Pro Asn Arg Tyr Phe Asp Val Ala Ile
            355             360             365

Ala Glu Gln His Ala Val Thr Leu Ala Ala Gly Gln Ala Cys Gln Gly
        370             375             380

Ala Lys Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly Tyr
385             390             395             400

Asp Gln Leu Ile His Asp Val Ala Leu Gln Asn Leu Asp Met Leu Phe
            405             410             415

Ala Leu Asp Arg Ala Gly Leu Val Gly Pro Asp Gly Pro Thr His Ala
            420             425             430
```

8

```
Gly Ala Phe Asp Tyr Ser Tyr Met Arg Cys Ile Pro Asn Met Leu Ile
        435             440             445

Met Ala Pro Ala Asp Glu Asn Glu Cys Arg Gln Met Leu Thr Thr Gly
        450             455             460

Phe Gln His His Gly Pro Ala Ser Val Arg Tyr Pro Arg Gly Lys Gly
465             470             475             480

Pro Gly Ala Ala Ile Asp Pro Thr Leu Thr Ala Leu Glu Ile Gly Lys
            485             490             495

Ala Glu Val Arg His His Gly Ser Arg Ile Ala Ile Leu Ala Trp Gly
        500             505             510

Ser Met Val Thr Pro Ala Val Glu Ala Gly Lys Gln Leu Gly Ala Thr
        515             520             525

Val Val Asn Met Arg Phe Val Lys Pro Phe Asp Gln Ala Leu Val Leu
        530             535             540

Glu Leu Ala Arg Thr His Asp Val Phe Val Thr Val Glu Glu Asn Val
545             550             555             560

Ile Ala Gly Gly Ala Gly Ser Ala Ile Asn Thr Phe Leu Gln Ala Gln
            565             570             575

Lys Val Leu Met Pro Val Cys Asn Ile Gly Leu Pro Asp Arg Phe Val
            580             585             590

Glu Gln Gly Ser Arg Glu Glu Leu Leu Ser Leu Val Gly Leu Asp Ser
        595             600             605

Lys Gly Ile Leu Ala Thr Ile Glu Gln Phe Cys Ala
    610             615             620


<210>   7
<211>   1182
<212>   DNA
<213>   Methylomonas 16a

<400>   7
atgaaaggta tttgcatatt gggcgctacc ggttcgatcg gtgtcagcac gctggatgtc     60

gttgccaggc atccggataa atatcaagtc gttgcgctga ccgccaacgg caatatcgac    120

gcattgtatg aacaatgcct ggcccaccat ccggagtatg cggtggtggt catggaaagc    180
```

9

```
aaggtagcag  agttcaaaca  gcgcattgcc  gcttcgccgg  tagcggatat  caaggtcttg      240

tcgggtagcg  aggccttgca  acaggtggcc  acgctggaaa  acgtcgatac  ggtgatggcg      300

gctatcgtcg  gcgcggccgg  attgttgccg  accttggccg  cggccaaggc  cggcaaaacc      360

gtgctgttgg  ccaacaagga  agccttggtg  atgtcgggac  aaatcttcat  gcaggccgtc      420

agcgattccg  gcgctgtgtt  gctgccgata  gacagcgagc  acaacgccat  ctttcagtgc      480

atgccggcgg  gttatacgcc  aggccataca  gccaaacagg  cgcgccgcat  tttattgacc      540

gcttccggtg  gcccatttcg  acggacgccg  atagaaacgt  tgtccagcgt  cacgccggat      600

caggccgttg  cccatcctaa  atgggacatg  gggcgcaaga  tttcggtcga  ttccgccacc      660

atgatgaaca  aaggtctcga  actgatcgaa  gcctgcttgt  tgttcaacat  ggagcccgac      720

cagattgaag  tcgtcattca  tccgcagagc  atcattcatt  cgatggtgga  ctatgtcgat      780

ggttcggttt  tggcgcagat  gggtaatccc  gacatgcgca  cgccgatagc  gcacgcgatg      840

gcctggccgg  aacgctttga  ctctggtgtg  gcgccgctgg  atattttcga  agtagggcac      900

atggatttcg  aaaaacccga  cttgaaacgg  tttccttgtc  tgagattggc  ttatgaagcc      960

atcaagtctg  gtggaattat  gccaacggta  ttgaacgcag  ccaatgaaat  tgctgtcgaa     1020

gcgttttta a  atgaagaagt  caaattcact  gacatcgcgg  tcatcatcga  gcgcagcatg     1080

gcccagttta  aaccggacga  tgccggcagc  ctcgaattgg  ttttgcaggc  cgatcaagat     1140

gcgcgcgagg  tggctagaga  catcatcaag  accttggtag  ct                        1182


<210>   8
<211>   394
<212>   PRT
<213>   Methylomonas 16a

<400>   8

Met Lys Gly Ile Cys Ile Leu Gly Ala Thr Gly Ser Ile Gly Val Ser
1               5                   10                  15


Thr Leu Asp Val Val Ala Arg His Pro Asp Lys Tyr Gln Val Val Ala
            20                  25                  30


Leu Thr Ala Asn Gly Asn Ile Asp Ala Leu Tyr Glu Gln Cys Leu Ala
        35                  40                  45


His His Pro Glu Tyr Ala Val Val Val Met Glu Ser Lys Val Ala Glu
    50                  55                  60


Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile Lys Val Leu
65                  70                  75                  80
```

10

```
Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu Asn Val Asp
              85                  90                  95

Thr Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu
            100                 105                 110

Ala Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn Lys Glu Ala
            115                 120                 125

Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser Asp Ser Gly
    130                 135                 140

Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile Phe Gln Cys
145                 150                 155                 160

Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln Ala Arg Arg
                165                 170                 175

Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr Pro Ile Glu
            180                 185                 190

Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His Pro Lys Trp
        195                 200                 205

Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met Met Asn Lys
    210                 215                 220

Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met Glu Pro Asp
225                 230                 235                 240

Gln Ile Glu Val Val Ile His Pro Gln Ser Ile Ile His Ser Met Val
                245                 250                 255

Asp Tyr Val Asp Gly Ser Val Leu Ala Gln Met Gly Asn Pro Asp Met
                260                 265                 270

Arg Thr Pro Ile Ala His Ala Met Ala Trp Pro Glu Arg Phe Asp Ser
        275                 280                 285

Gly Val Ala Pro Leu Asp Ile Phe Glu Val Gly His Met Asp Phe Glu
    290                 295                 300

Lys Pro Asp Leu Lys Arg Phe Pro Cys Leu Arg Leu Ala Tyr Glu Ala
305                 310                 315                 320
```

11

Ile Lys Ser Gly Gly Ile Met Pro Thr Val Leu Asn Ala Ala Asn Glu
            325   330   335

Ile Ala Val Glu Ala Phe Leu Asn Glu Glu Val Lys Phe Thr Asp Ile
            340   345   350

Ala Val Ile Ile Glu Arg Ser Met Ala Gln Phe Lys Pro Asp Asp Ala
            355   360   365

Gly Ser Leu Glu Leu Val Leu Gln Ala Asp Gln Asp Ala Arg Glu Val
            370   375   380

Ala Arg Asp Ile Ile Lys Thr Leu Val Ala
385   390

<210> 9
<211> 693
<212> DNA
<213> Methylomonas 16a

<400> 9
atgaacccaa ccatccaatg ctgggccgtc gtgcccgcag ccggcgtcgg caaacgcatg   60

caagccgatc gccccaaaca atatttaccg cttgccggta aaacggtcat cgaacacaca   120

ctgactcgac tacttgagtc cgacgccttc caaaaagttg cggtggcgat ttccgtcgaa   180

gacccttatt ggcctgaact gtccatagcc aaacaccccg acatcatcac cgcgcctggc   240

ggcaaggaac gcgccgactc ggtgctgtct gcactgaagg ctttagaaga tatagccagc   300

gaaaatgatt gggtgctggt acacgacgcc gcccgcccct gcttgacggg cagcgacatc   360

caccttcaaa tcgatacctt aaaaaatgac ccggtcggcg catcctggc cttgagttcg   420

cacgacacat tgaaacacgt ggatggtgac acgatcaccg caaccataga cagaaagcac   480

gtctggcgcg ccttgacgcc gcaaatgttc aaatacggca tgttgcgcga cgcgttgcaa   540

cgaaccgaag gcaatccggc cgtcaccgac gaagccagtg cgctggaact tttgggccat   600

aaacccaaaa tcgtggaagg ccgcccggac aacatcaaaa tcacccgccc ggaagatttg   660

gccctggcac aattttatat ggagcaacaa gca   693

<210> 10
<211> 231
<212> PRT
<213> Methylomonas 16a

12

<400> 10

Met Asn Pro Thr Ile Gln Cys Trp Ala Val Val Pro Ala Ala Gly Val
1   5   10   15

Gly Lys Arg Met Gln Ala Asp Arg Pro Lys Gln Tyr Leu Pro Leu Ala
            20   25   30

Gly Lys Thr Val Ile Glu His Thr Leu Thr Arg Leu Leu Glu Ser Asp
            35   40   45

Ala Phe Gln Lys Val Ala Val Ala Ile Ser Val Glu Asp Pro Tyr Trp
        50   55   60

Pro Glu Leu Ser Ile Ala Lys His Pro Asp Ile Ile Thr Ala Pro Gly
65   70   75   80

Gly Lys Glu Arg Ala Asp Ser Val Leu Ser Ala Leu Lys Ala Leu Glu
                85   90   95

Asp Ile Ala Ser Glu Asn Asp Trp Val Leu Val His Asp Ala Ala Arg
            100   105   110

Pro Cys Leu Thr Gly Ser Asp Ile His Leu Gln Ile Asp Thr Leu Lys
        115   120   125

Asn Asp Pro Val Gly Gly Ile Leu Ala Leu Ser Ser His Asp Thr Leu
        130   135   140

Lys His Val Asp Gly Asp Thr Ile Thr Ala Thr Ile Asp Arg Lys His
145   150   155   160

Val Trp Arg Ala Leu Thr Pro Gln Met Phe Lys Tyr Gly Met Leu Arg
            165   170   175

Asp Ala Leu Gln Arg Thr Glu Gly Asn Pro Ala Val Thr Asp Glu Ala
            180   185   190

Ser Ala Leu Glu Leu Leu Gly His Lys Pro Lys Ile Val Glu Gly Arg
        195   200   205

Pro Asp Asn Ile Lys Ile Thr Arg Pro Glu Asp Leu Ala Leu Ala Gln
        210   215   220

Phe Tyr Met Glu Gln Gln Ala
225   230

13

<210> 11
<211> 855
<212> DNA
<213> Methylomonas 16a

<400> 11
atggattatg cggctgggtg gggcgaaaga tggcctgctc cggcaaaatt gaacttaatg   60

ttgaggatta ccggtcgcag gccagatggc tatcatctgt tgcaaacggt gtttcaaatg   120

ctcgatctat gcgattggtt gacgtttcat ccggttgatg atggccgcgt gacgctgcga   180

aatccaatct ccggcgttcc agagcaggat gacttgactg ttcgggcggc taatttgttg   240

aagtctcata ccggctgtgt gcgcggagtt tgtatcgata tcgagaaaaa tctgcctatg   300

ggtggtggtt tgggtggtgg aagttccgat gctgctacaa ccttggtagt tctaaatcgg   360

ctttggggct tgggcttgtc gaagcgtgag ttgatggatt tgggcttgag gcttggtgcc   420

gatgtgcctg tgtttgtgtt tggttgttcg gcctggggcg aaggtgtgag cgaggatttg   480

caggcaataa cgttgccgga acaatggttt gtcatcatta accggattg ccatgtgaat   540

actggagaaa tttttctgc agaaaatttg acaggaata gtgcagtcgt tacaatgagc   600

gactttcttg cagggataa tcggaatgat tgttcggaag tggtttgcaa gttatatcga   660

ccggtgaaag atgcaatcga tgcgttgtta tgctatgcgg aagcgagatt gacggggacc   720

ggtgcatgtg tgttcgctca gttttgtaac aaggaagatg ctgagagtgc gttagaagga   780

ttgaaagatc ggtggctggt gttcttggct aaaggcttga atcagtctgc gctctacaag   840

aaattagaac aggga   855

<210> 12
<211> 285
<212> PRT
<213> Methylomonas 16a

<400> 12

Met Asp Tyr Ala Ala Gly Trp Gly Glu Arg Trp Pro Ala Pro Ala Lys
1   5   10   15

Leu Asn Leu Met Leu Arg Ile Thr Gly Arg Arg Pro Asp Gly Tyr His
            20   25   30

Leu Leu Gln Thr Val Phe Gln Met Leu Asp Leu Cys Asp Trp Leu Thr
        35   40   45

Phe His Pro Val Asp Asp Gly Arg Val Thr Leu Arg Asn Pro Ile Ser
    50   55   60

14

```
Gly Val Pro Glu Gln Asp Asp Leu Thr Val Arg Ala Ala Asn Leu Leu
65                  70              75                  80

Lys Ser His Thr Gly Cys Val Arg Gly Val Cys Ile Asp Ile Glu Lys
                85                  90              95

Asn Leu Pro Met Gly Gly Gly Leu Gly Gly Ser Ser Asp Ala Ala
            100             105             110

Thr Thr Leu Val Val Leu Asn Arg Leu Trp Gly Leu Gly Leu Ser Lys
            115             120             125

Arg Glu Leu Met Asp Leu Gly Leu Arg Leu Gly Ala Asp Val Pro Val
    130             135             140

Phe Val Phe Gly Cys Ser Ala Trp Gly Glu Gly Val Ser Glu Asp Leu
145             150             155             160

Gln Ala Ile Thr Leu Pro Glu Gln Trp Phe Val Ile Ile Lys Pro Asp
            165             170             175

Cys His Val Asn Thr Gly Glu Ile Phe Ser Ala Glu Asn Leu Thr Arg
            180             185             190

Asn Ser Ala Val Val Thr Met Ser Asp Phe Leu Ala Gly Asp Asn Arg
    195             200             205

Asn Asp Cys Ser Glu Val Val Cys Lys Leu Tyr Arg Pro Val Lys Asp
    210             215             220

Ala Ile Asp Ala Leu Leu Cys Tyr Ala Glu Ala Arg Leu Thr Gly Thr
225             230             235             240

Gly Ala Cys Val Phe Ala Gln Phe Cys Asn Lys Glu Asp Ala Glu Ser
            245             250             255

Ala Leu Glu Gly Leu Lys Asp Arg Trp Leu Val Phe Leu Ala Lys Gly
            260             265             270

Leu Asn Gln Ser Ala Leu Tyr Lys Lys Leu Glu Gln Gly
        275             280             285


<210>   13
<211>   471
```

15

<212> DNA
<213> Methylomonas 16a

<400> 13

```
atgatacgcg taggcatggg ttacgacgtg caccgtttca acgacggcga ccacatcatt      60

ttgggcggcg tcaaaatccc ttatgaaaaa ggcctggaag cccattccga cggcgacgtg     120

gtgctgcacg cattggccga cgccatcttg ggagccgccg ctttgggcga catcggcaaa     180

catttcccgg acaccgaccc caatttcaag ggcgccgaca gcagggtgct actgcgccac     240

gtgtacggca tcgtcaagga aaaaggctat aaactggtca cgccgacgt gaccatcatc      300

gctcaggcgc cgaagatgct gccacacgtg cccggcatgc gcgccaacat tgccgccgat     360

ctggaaaccg atgtcgattt cattaatgta aaagccacga cgaccgagaa actgggcttt     420

gagggccgta aggaaggcat cgccgtgcag gctgtggtgt tgatagaacg c             471
```

<210> 14
<211> 157
<212> PRT
<213> Methylomonas 16a

<400> 14

```
Met Ile Arg Val Gly Met Gly Tyr Asp Val His Arg Phe Asn Asp Gly
1               5                   10                  15


Asp His Ile Ile Leu Gly Gly Val Lys Ile Pro Tyr Glu Lys Gly Leu
            20                  25                  30


Glu Ala His Ser Asp Gly Asp Val Val Leu His Ala Leu Ala Asp Ala
        35                  40                  45


Ile Leu Gly Ala Ala Ala Leu Gly Asp Ile Gly Lys His Phe Pro Asp
    50                  55                  60


Thr Asp Pro Asn Phe Lys Gly Ala Asp Ser Arg Val Leu Leu Arg His
65                  70                  75                  80


Val Tyr Gly Ile Val Lys Glu Lys Gly Tyr Lys Leu Val Asn Ala Asp
                85                  90                  95


Val Thr Ile Ile Ala Gln Ala Pro Lys Met Leu Pro His Val Pro Gly
            100                 105                 110


Met Arg Ala Asn Ile Ala Ala Asp Leu Glu Thr Asp Val Asp Phe Ile
        115                 120                 125
```

16

Asn Val Lys Ala Thr Thr Thr Glu Lys Leu Gly Phe Glu Gly Arg Lys
        130   135   140

Glu Gly Ile Ala Val Gln Ala Val Val Leu Ile Glu Arg
145   150   155

<210> 15
<211> 1632
<212> DNA
<213> Methylomonas 16a

<400> 15
atgacaaaat tcatctttat caccggcggc gtggtgtcat ccttgggaaa agggatagcc   60

gcctcctccc tggcggcgat tctggaagac cgcggcctca agtcactat cacaaaactc   120

gatccctaca tcaacgtcga ccccggcacc atgagcccgt tcaacacgg cgaggtgttc   180

gtgaccgaag acggtgccga aaccgatttg gaccttggcc attacgaacg ttttttgaaa   240

accacgatga ccaagaaaaa caacttcacc accggtcagg tttacgagca ggtattacgc   300

aacgagcgca aggtgatta tcttggcgcg accgtgcaag tcattccaca tatcaccgac   360

gaaatcaaac gccgggtgta tgaaagcgcc gaagggaaag atgtggcatt gatcgaagtc   420

ggcggcacgg tgggcgacat cgaatcgtta ccgtttctgg aaaccatacg ccagatgggc   480

gtggaactgg gtcgtgaccg cgccttgttc attcatttga cgctggtgcc ttacatcaaa   540

tcggccggcg aactgaaaac caagcccacc cagcattcgg tcaaagaact gcgcaccatc   600

gggattcagc cggacatttt gatctgtcgt tcagaacaac cgatcccggc cagtgaacgc   660

cgcaagatcg cgctatttac caatgtcgcc gaaaaggcgg tgatttccgc gatcgatgcc   720

gacaccattt accgcattcc gctattgctg cgcgaacaag gcctggacga cctggtggtc   780

gatcagttgc gcctggacgt accagcggcg gatttatcgg cctgggaaaa ggtcgtcgat   840

ggcctgactc atccgaccga cgaagtcagc attgcgatcg tcggtaaata tgtcgaccac   900

accgatgcct acaaatcgct gaatgaagcc ctgattcatg ccggcattca cacgcgccac   960

aaggtgcaaa tcagctacat cgactccgaa accatagaag ccgaaggcac cgccaaattg   1020

aaaaacgtcg atgcgatcct ggtgccgggt ggtttcggcg aacgcggcgt ggaaggcaag   1080

atttctaccg tgcgttttgc ccgcgagaac aaaatcccgt atttgggcat ttgcttgggc   1140

atgcaatcgg cggtaatcga attcgcccgc aacgtggttg cctggaagg cgcgcacagc   1200

accgaattcc tgccgaaatc gccacaccct gtgatcggct gatcaccga atggatggac   1260

gaagccggcg aactggtcac acgcgacgaa gattccgatc tgggcggcac gatgcgtctg   1320

ggcgcgcaaa aatgccgcct gaaggctgat tccttggctt ttcagttgta tcaaaaagac   1380

17

```
gtcatcaccg agcgtcaccg ccaccgctac gaattcaaca atcaatattt aaaacaactg      1440

gaagcggccg gcatgaaatt ttccggtaaa tcgctggacg ccgcctggt ggagatcatc        1500

gagctacccg aacacccctg gttcctggcc tgccagttcc atcccgaatt cacctcgacg       1560

ccgcgtaacg gccacgccct attttcgggc ttcgtcgaag cggccgccaa acacaaaaca       1620

caaggcacag ca                                                          1632
```

<210> 16
<211> 544
<212> PRT
<213> Methylomonas 16a

<400> 16

```
Met Thr Lys Phe Ile Phe Ile Thr Gly Gly Val Val Ser Ser Leu Gly
1               5                   10                  15


Lys Gly Ile Ala Ala Ser Ser Leu Ala Ala Ile Leu Glu Asp Arg Gly
                20                  25                  30


Leu Lys Val Thr Ile Thr Lys Leu Asp Pro Tyr Ile Asn Val Asp Pro
            35                  40                  45


Gly Thr Met Ser Pro Phe Gln His Gly Glu Val Phe Val Thr Glu Asp
        50                  55                  60


Gly Ala Glu Thr Asp Leu Asp Leu Gly His Tyr Glu Arg Phe Leu Lys
65                  70                  75                  80


Thr Thr Met Thr Lys Lys Asn Asn Phe Thr Thr Gly Gln Val Tyr Glu
                85                  90                  95


Gln Val Leu Arg Asn Glu Arg Lys Gly Asp Tyr Leu Gly Ala Thr Val
            100                 105                 110


Gln Val Ile Pro His Ile Thr Asp Glu Ile Lys Arg Arg Val Tyr Glu
            115                 120                 125


Ser Ala Glu Gly Lys Asp Val Ala Leu Ile Glu Val Gly Gly Thr Val
        130                 135                 140


Gly Asp Ile Glu Ser Leu Pro Phe Leu Glu Thr Ile Arg Gln Met Gly
145                 150                 155                 160


Val Glu Leu Gly Arg Asp Arg Ala Leu Phe Ile His Leu Thr Leu Val
                165                 170                 175
```

18

Pro Tyr Ile Lys Ser Ala Gly Glu Leu Lys Thr Lys Pro Thr Gln His
        180   185   190

Ser Val Lys Glu Leu Arg Thr Ile Gly Ile Gln Pro Asp Ile Leu Ile
        195   200   205

Cys Arg Ser Glu Gln Pro Ile Pro Ala Ser Glu Arg Arg Lys Ile Ala
     210   215   220

Leu Phe Thr Asn Val Ala Glu Lys Ala Val Ile Ser Ala Ile Asp Ala
225   230   235   240

Asp Thr Ile Tyr Arg Ile Pro Leu Leu Leu Arg Glu Gln Gly Leu Asp
           245   250   255

Asp Leu Val Val Asp Gln Leu Arg Leu Asp Val Pro Ala Ala Asp Leu
        260   265   270

Ser Ala Trp Glu Lys Val Val Asp Gly Leu Thr His Pro Thr Asp Glu
        275   280   285

Val Ser Ile Ala Ile Val Gly Lys Tyr Val Asp His Thr Asp Ala Tyr
        290   295   300

Lys Ser Leu Asn Glu Ala Leu Ile His Ala Gly Ile His Thr Arg His
305   310   315   320

Lys Val Gln Ile Ser Tyr Ile Asp Ser Glu Thr Ile Glu Ala Glu Gly
           325   330   335

Thr Ala Lys Leu Lys Asn Val Asp Ala Ile Leu Val Pro Gly Gly Phe
        340   345   350

Gly Glu Arg Gly Val Glu Gly Lys Ile Ser Thr Val Arg Phe Ala Arg
        355   360   365

Glu Asn Lys Ile Pro Tyr Leu Gly Ile Cys Leu Gly Met Gln Ser Ala
        370   375   380

Val Ile Glu Phe Ala Arg Asn Val Val Gly Leu Glu Gly Ala His Ser
385   390   395   400

Thr Glu Phe Leu Pro Lys Ser Pro His Pro Val Ile Gly Leu Ile Thr
        405   410   415

```
Glu Trp Met Asp Glu Ala Gly Glu Leu Val Thr Arg Asp Glu Asp Ser
        420             425             430

Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Gln Lys Cys Arg Leu Lys
        435             440             445

Ala Asp Ser Leu Ala Phe Gln Leu Tyr Gln Lys Asp Val Ile Thr Glu
    450             455             460

Arg His Arg His Arg Tyr Glu Phe Asn Asn Gln Tyr Leu Lys Gln Leu
465             470             475             480

Glu Ala Ala Gly Met Lys Phe Ser Gly Lys Ser Leu Asp Gly Arg Leu
            485             490             495

Val Glu Ile Ile Glu Leu Pro Glu His Pro Trp Phe Leu Ala Cys Gln
        500             505             510

Phe His Pro Glu Phe Thr Ser Thr Pro Arg Asn Gly His Ala Leu Phe
        515             520             525

Ser Gly Phe Val Glu Ala Ala Ala Lys His Lys Thr Gln Gly Thr Ala
    530             535             540

<210>   17
<211>   954
<212>   DNA
<213>   Methylomonas 16a

<400>   17
atgcaaatcg tactcgcaaa cccccgtgga ttctgtgccg gcgtggaccg ggccattgaa     60

attgtcgatc aagccatcga agcctttggt gcgccgattt atgtgcggca cgaggtggtg    120

cataaccgca ccgtggtcga tggactgaaa caaaaaggtg cggtgttcat cgaggaacta    180

agcgatgtgc cggtgggttc ctacttgatt ttcagcgcgc acggcgtatc caaggaggtg    240

caacaggaag ccgaggagcg ccagttgacg gtattcgatg cgacttgtcc gctggtgacc    300

aaagtgcaca tgcaggttgc caagcatgcc aaacagggcc gagaagtgat tttgatcggc    360

cacgccggtc atccggaagt ggaaggcacg atgggccagt atgaaaaatg caccgaaggc    420

ggcggcattt atctggtcga aactccggaa gacgtacgca atttgaaagt caacaatccc    480

aatgatctgg cctatgtgac gcagacgacc ttgtcgatga ccgacaccaa ggtcatggtg    540

gatgcgttac gcgaacaatt tccgtccatt aaggagcaaa aaaggacga tatttgttac    600
```

20

```
gcgacgcaaa accgtcagga tgcggtgcat gatctggcca agatttccga cctgattctg    660

gttgtcggct ctcccaatag ttcgaattcc aaccgtttgc gtgaaatcgc cgtgcaactc    720

ggtaaacccg cttatttgat cgatacttac caggatttga agcaagattg gctggaggga    780

attgaagtag tcggggttac cgcgggcgct tcggcgccgg aagtgttggt gcaggaagtg    840

atcgatcaac tgaaggcatg gggcggcgaa accacttcgg tcagagaaaa cagcggcatc    900

gaggaaaagg tagtctttc gattcccaag gagttgaaaa acatatgca agcg            954
```

<210> 18
<211> 318
<212> PRT
<213> Methylomonas 16a

<400> 18

```
Met Gln Ile Val Leu Ala Asn Pro Arg Gly Phe Cys Ala Gly Val Asp
1               5                   10                  15


Arg Ala Ile Glu Ile Val Asp Gln Ala Ile Glu Ala Phe Gly Ala Pro
                20                  25                  30


Ile Tyr Val Arg His Glu Val Val His Asn Arg Thr Val Val Asp Gly
            35                  40                  45


Leu Lys Gln Lys Gly Ala Val Phe Ile Glu Glu Leu Ser Asp Val Pro
        50                  55                  60


Val Gly Ser Tyr Leu Ile Phe Ser Ala His Gly Val Ser Lys Glu Val
65                  70                  75                  80


Gln Gln Glu Ala Glu Glu Arg Gln Leu Thr Val Phe Asp Ala Thr Cys
                85                  90                  95


Pro Leu Val Thr Lys Val His Met Gln Val Ala Lys His Ala Lys Gln
                100                 105                 110


Gly Arg Glu Val Ile Leu Ile Gly His Ala Gly His Pro Glu Val Glu
            115                 120                 125


Gly Thr Met Gly Gln Tyr Glu Lys Cys Thr Glu Gly Gly Gly Ile Tyr
            130                 135                 140


Leu Val Glu Thr Pro Glu Asp Val Arg Asn Leu Lys Val Asn Asn Pro
145                 150                 155                 160
```

21

```
Asn Asp Leu Ala Tyr Val Thr Gln Thr Thr Leu Ser Met Thr Asp Thr
            165                 170                 175

Lys Val Met Val Asp Ala Leu Arg Glu Gln Phe Pro Ser Ile Lys Glu
            180                 185                 190

Gln Lys Lys Asp Asp Ile Cys Tyr Ala Thr Gln Asn Arg Gln Asp Ala
            195                 200                 205

Val His Asp Leu Ala Lys Ile Ser Asp Leu Ile Leu Val Val Gly Ser
    210                 215                 220

Pro Asn Ser Ser Asn Ser Asn Arg Leu Arg Glu Ile Ala Val Gln Leu
225                 230                 235                 240

Gly Lys Pro Ala Tyr Leu Ile Asp Thr Tyr Gln Asp Leu Lys Gln Asp
            245                 250                 255

Trp Leu Glu Gly Ile Glu Val Val Gly Val Thr Ala Gly Ala Ser Ala
            260                 265                 270

Pro Glu Val Leu Val Gln Glu Val Ile Asp Gln Leu Lys Ala Trp Gly
            275                 280                 285

Gly Glu Thr Thr Ser Val Arg Glu Asn Ser Gly Ile Glu Glu Lys Val
    290                 295                 300

Val Phe Ser Ile Pro Lys Glu Leu Lys Lys His Met Gln Ala
305                 310                 315
```

<210> 19
<211> 891
<212> DNA
<213> Methylomonas 16a

<400> 19

```
atgagtaaat tgaaagccta cctgaccgtc tgccaagaac gcgtcgagcg cgcgctggac      60

gcccgtctgc ctgccgaaaa catactgcca caaaccttgc atcaggccat gcgctattcc     120

gtattgaacg gcggcaaacg cacccggccc ttgttgactt atgcgaccgg tcaggctttg     180

ggcttgccgg aaaacgtgct ggatgcgccg gcttgcgcgg tagaattcat ccatgtgtat     240

tcgctgattc acgacgatct gccggccatg gacaacgatg atctgcgccg cggcaaaccg     300

acctgtcaca aggcttacga cgaggccacc gccattttgg ccggcgacgc actgcaggcg     360

ctggcctttg aagttctggc caacgacccc ggcatcaccg tcgatgcccc ggctcgcctg     420
```

22

```
aaaatgatca cggctttgac ccgcgccagc ggctctcaag gcatggtggg cggtcaagcc    480

atcgatctcg gctccgtcgg ccgcaaattg acgctgccgg aactcgaaaa catgcatatc    540

cacaagactg gcgccctgat ccgcgccagc gtcaatctgg cggcattatc caaacccgat    600

ctggatactt gcgtcgccaa gaaactggat cactatgcca aatgcatagg cttgtcgttc    660

caggtcaaag acgacattct cgacatcgaa gccgacaccg cgacactcgg caagactcag    720

ggcaaggaca tcgataacga caaaccgacc taccctgcgc tattgggcat ggctggcgcc    780

aaacaaaaag cccaggaatt gcacgaacaa gcagtcgaaa gcttaacggg atttggcagc    840

gaagccgacc tgctgcgcga actatcgctt tacatcatcg agcgcacgca c             891
```

<210>   20
<211>   297
<212>   PRT
<213>   Methylomonas 16a

<400>   20

```
Met Ser Lys Leu Lys Ala Tyr Leu Thr Val Cys Gln Glu Arg Val Glu
1               5                   10                  15


Arg Ala Leu Asp Ala Arg Leu Pro Ala Glu Asn Ile Leu Pro Gln Thr
            20                  25                  30


Leu His Gln Ala Met Arg Tyr Ser Val Leu Asn Gly Gly Lys Arg Thr
            35                  40                  45


Arg Pro Leu Leu Thr Tyr Ala Thr Gly Gln Ala Leu Gly Leu Pro Glu
        50                  55                  60


Asn Val Leu Asp Ala Pro Ala Cys Ala Val Glu Phe Ile His Val Tyr
65                  70                  75                  80


Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp Leu Arg
                85                  90                  95


Arg Gly Lys Pro Thr Cys His Lys Ala Tyr Asp Glu Ala Thr Ala Ile
                100                 105                 110


Leu Ala Gly Asp Ala Leu Gln Ala Leu Ala Phe Glu Val Leu Ala Asn
            115                 120                 125


Asp Pro Gly Ile Thr Val Asp Ala Pro Ala Arg Leu Lys Met Ile Thr
            130                 135                 140
```

23

```
Ala Leu Thr Arg Ala Ser Gly Ser Gln Gly Met Val Gly Gly Gln Ala
145                 150                 155                 160


Ile Asp Leu Gly Ser Val Gly Arg Lys Leu Thr Leu Pro Glu Leu Glu
                165                 170                 175


Asn Met His Ile His Lys Thr Gly Ala Leu Ile Arg Ala Ser Val Asn
                180                 185                 190


Leu Ala Ala Leu Ser Lys Pro Asp Leu Asp Thr Cys Val Ala Lys Lys
                195                 200                 205


Leu Asp His Tyr Ala Lys Cys Ile Gly Leu Ser Phe Gln Val Lys Asp
    210                 215                 220


Asp Ile Leu Asp Ile Glu Ala Asp Thr Ala Thr Leu Gly Lys Thr Gln
225                 230                 235                 240


Gly Lys Asp Ile Asp Asn Asp Lys Pro Thr Tyr Pro Ala Leu Leu Gly
                245                 250                 255


Met Ala Gly Ala Lys Gln Lys Ala Gln Glu Leu His Glu Gln Ala Val
                260                 265                 270


Glu Ser Leu Thr Gly Phe Gly Ser Glu Ala Asp Leu Leu Arg Glu Leu
                275                 280                 285


Ser Leu Tyr Ile Ile Glu Arg Thr His
    290                 295


<210>   21
<211>   1533
<212>   DNA
<213>   Methylomonas 16a

<400>   21
atggccaaca ccaaacacat catcatcgtc ggcgcgggtc ccggcggact ttgcgccggc      60

atgttgctga gccagcgcgg cttcaaggta tcgattttcg acaaacatgc agaaatcggc     120

ggccgcaacc gcccgatcaa catgaacggc tttaccttcg ataccggtcc gacattcttg     180

ttgatgaaag gcgtgctgga cgaaatgttc gaactgtgcg agcgccgtag cgaggattat     240

ctggaattcc tgccgctaag cccgatgtac cgcctgctgt cgacgaccg cgacatcttc      300

gtctattccg accgcgagaa catgcgcgcc gaattgcaac gggtattcga cgaaggcacg     360

gacggctacg aacagttcat ggaacaggaa cgcaaacgct caacgcgct gtatccctgc      420
```

24

```
atcacccgcg attattccag cctgaaatcc tttttgtcgc tggacttgat caaggccctg     480

ccgtggctgg cttttccgaa aagcgtgttc aataatctcg gccagtattt caaccaggaa     540

aaaatgcgcc tggccttttg ctttcagtcc aagtatctgg gcatgtcgcc gtgggaatgc     600

ccggcactgt ttacgatgct gccctatctg gagcacgaat acggcattta tcacgtcaaa     660

ggcggcctga accgcatcgc ggcggcgatg gcgcaagtga tcgcggaaaa cggcggcgaa     720

attcacttga acagcgaaat cgagtcgctg atcatcgaaa acggcgctgc caagggcgtc     780

aaattacaac atggcgcgga gctgcgcggc gacgaagtca tcatcaacgc ggattttgcc     840

cacgcgatga cgcatctggt caaaccgggc gtcttgaaaa atacaccccc ggaaaacctg     900

aagcagcgcg agtattcctg ttcgaccttc atgctgtatc tgggtttgga caagatttac     960

gatctgccgc accataccat cgtgtttgcc aaggattaca ccaccaatat ccgcaacatt    1020

ttcgacaaca aaaccctgac ggacgatttt tcgttttacg tgcaaaacgc cagcgccagc    1080

gacgacagcc tagcgccagc cggcaaatcg cgctgtacg tgctggtgcc gatgcccaac     1140

aacgacagcg cctggactg caggcgcat tgccaaaacg tgcgcgaaca ggtgttggac      1200

acgctgggcg cgcgactggg attgagcgac atcagagccc atatcgaatg cgaaaaaatc    1260

atcacgccgc aaacctggga aacggacgaa cacgtttaca agggcgccac tttcagtttg    1320

tcgcacaagt tcagccaaat gctgtactgg cggccgcaca accgtttcga ggaactggcc    1380

aattgctatc tggtcggcgg cggcacgcat cccggtagcg gtttgccgac catctacgaa    1440

tcggcgcgga tttcggccaa gctgatttcc cagaaacatc gggtgaggtt caaggacata    1500

gcacacagcg cctggctgaa aaaagccaaa gcc                                  1533
```

<210> 22
<211> 511
<212> PRT
<213> Methylomonas 16a

<400> 22

```
Met Ala Asn Thr Lys His Ile Ile Ile Val Gly Ala Gly Pro Gly Gly
1               5                   10                  15


Leu Cys Ala Gly Met Leu Leu Ser Gln Arg Gly Phe Lys Val Ser Ile
            20                  25                  30


Phe Asp Lys His Ala Glu Ile Gly Gly Arg Asn Arg Pro Ile Asn Met
        35                  40                  45


Asn Gly Phe Thr Phe Asp Thr Gly Pro Thr Phe Leu Leu Met Lys Gly
    50                  55                  60
```

25

```
Val Leu Asp Glu Met Phe Glu Leu Cys Glu Arg Arg Ser Glu Asp Tyr
65              70              75              80


Leu Glu Phe Leu Pro Leu Ser Pro Met Tyr Arg Leu Leu Tyr Asp Asp
            85              90              95


Arg Asp Ile Phe Val Tyr Ser Asp Arg Glu Asn Met Arg Ala Glu Leu
            100             105             110


Gln Arg Val Phe Asp Glu Gly Thr Asp Gly Tyr Glu Gln Phe Met Glu
            115             120             125


Gln Glu Arg Lys Arg Phe Asn Ala Leu Tyr Pro Cys Ile Thr Arg Asp
    130             135             140


Tyr Ser Ser Leu Lys Ser Phe Leu Ser Leu Asp Leu Ile Lys Ala Leu
145             150             155             160


Pro Trp Leu Ala Phe Pro Lys Ser Val Phe Asn Asn Leu Gly Gln Tyr
            165             170             175


Phe Asn Gln Glu Lys Met Arg Leu Ala Phe Cys Phe Gln Ser Lys Tyr
            180             185             190


Leu Gly Met Ser Pro Trp Glu Cys Pro Ala Leu Phe Thr Met Leu Pro
            195             200             205


Tyr Leu Glu His Glu Tyr Gly Ile Tyr His Val Lys Gly Gly Leu Asn
    210             215             220


Arg Ile Ala Ala Ala Met Ala Gln Val Ile Ala Glu Asn Gly Gly Glu
225             230             235             240


Ile His Leu Asn Ser Glu Ile Glu Ser Leu Ile Ile Glu Asn Gly Ala
            245             250             255


Ala Lys Gly Val Lys Leu Gln His Gly Ala Glu Leu Arg Gly Asp Glu
            260             265             270


Val Ile Ile Asn Ala Asp Phe Ala His Ala Met Thr His Leu Val Lys
            275             280             285


Pro Gly Val Leu Lys Lys Tyr Thr Pro Glu Asn Leu Lys Gln Arg Glu
    290             295             300
```

26

```
Tyr Ser Cys Ser Thr Phe Met Leu Tyr Leu Gly Leu Asp Lys Ile Tyr
305             310             315             320

Asp Leu Pro His His Thr Ile Val Phe Ala Lys Asp Tyr Thr Thr Asn
                325             330             335

Ile Arg Asn Ile Phe Asp Asn Lys Thr Leu Thr Asp Asp Phe Ser Phe
            340             345             350

Tyr Val Gln Asn Ala Ser Ala Ser Asp Asp Ser Leu Ala Pro Ala Gly
            355             360             365

Lys Ser Ala Leu Tyr Val Leu Val Pro Met Pro Asn Asn Asp Ser Gly
    370             375             380

Leu Asp Trp Gln Ala His Cys Gln Asn Val Arg Glu Gln Val Leu Asp
385             390             395             400

Thr Leu Gly Ala Arg Leu Gly Leu Ser Asp Ile Arg Ala His Ile Glu
            405             410             415

Cys Glu Lys Ile Ile Thr Pro Gln Thr Trp Glu Thr Asp Glu His Val
            420             425             430

Tyr Lys Gly Ala Thr Phe Ser Leu Ser His Lys Phe Ser Gln Met Leu
            435             440             445

Tyr Trp Arg Pro His Asn Arg Phe Glu Glu Leu Ala Asn Cys Tyr Leu
    450             455             460

Val Gly Gly Gly Thr His Pro Gly Ser Gly Leu Pro Thr Ile Tyr Glu
465             470             475             480

Ser Ala Arg Ile Ser Ala Lys Leu Ile Ser Gln Lys His Arg Val Arg
            485             490             495

Phe Lys Asp Ile Ala His Ser Ala Trp Leu Lys Lys Ala Lys Ala
            500             505             510


<210>  23
<211>  1491
<212>  DNA
<213>  Methylomonas 16a
```

27

<400> 23

```
atgaactcaa atgacaacca acgcgtgatc gtgatcggcg ccggcctcgg cggcctgtcc      60

gccgctattt cgctggccac ggccggcttt tccgtgcaac tcatcgaaaa aaacgacaag     120

gtcggcggca agctcaacat catgaccaaa gacggcttta ccttcgatct ggggccgtcc     180

attttgacga tgccgcacat ctttgaggcc ttgttcacag gggccggcaa aaacatggcc     240

gattacgtgc aaatccagaa agtcgaaccg cactggcgca atttcttcga ggacggtagc     300

gtgatcgact tgtgcgaaga cgccgaaacc cagcgccgcg agctggataa acttggcccc     360

ggcacttacg cgcaattcca gcgctttctg gactattcga aaaacctctg cacggaaacc     420

gaagccggtt acttcgccaa gggcctggac ggcttttggg atttactcaa gttttacggc     480

ccgctccgca gcctgctgag tttcgacgtc ttccgcagca tggaccaggg cgtgcgccgc     540

tttatttccg atcccaagtt ggtcgaaatc ctgaattact catcaaata cgtcggctcc     600

tcgccttacg atgcgcccgc cttgatgaac ctgctgcctt acattcaata tcattacggc     660

ctgtggtacg tgaaaggcgg catgtatggc atggcgcagg ccatggaaaa actggccgtg     720

gaattgggcg tcgagattcg tttagatgcc gaggtgtcgg aaatccaaaa acaggacggc     780

agagcctgcg ccgtaaagtt ggcgaacggc gacgtgctgc cggccgacat cgtggtgtcg     840

aacatggaag tgattccggc gatggaaaaa ctgctgcgca gcccggccag cgaactgaaa     900

aaaatgcagc gcttcgagcc tagctgttcc ggcctggtgc tgcacttggg cgtggacagg     960

ctgtatccgc aactggcgca ccacaatttc ttttattccg atcatccgcg cgaacatttc    1020

gatgcggtat tcaaaagcca tcgcctgtcg gacgatccga ccatttatct ggtcgcgccg    1080

tgcaagaccg accccgccca ggcgccggcc ggctgcgaga tcatcaaaat cctgccccat    1140

atcccgcacc tcgaccccga caaactgctg accgccgagg attattcagc cttgcgcgag    1200

cgggtgctgg tcaaactcga acgcatgggc ctgacggatt tacgccaaca catcgtgacc    1260

gaagaatact ggacgccgct ggatattcag gccaaatatt attcaaacca gggctcgatt    1320

tacggcgtgg tcgccgaccg cttcaaaaac ctgggtttca aggcacctca acgcagcagc    1380

gaattatcca atctgtattt cgtcggcggc agcgtcaatc ccggcggcgg catgccgatg    1440

gtgacgctgt ccgggcaatt ggtgagggac aagattgtgg cggatttgca a            1491
```

<210>   24
<211>   497
<212>   PRT
<213>   Methylomonas 16a

<400> 24

```
Met Asn Ser Asn Asp Asn Gln Arg Val Ile Val Ile Gly Ala Gly Leu
1               5                   10                  15

Gly Gly Leu Ser Ala Ala Ile Ser Leu Ala Thr Ala Gly Phe Ser Val
            20                  25                  30

Gln Leu Ile Glu Lys Asn Asp Lys Val Gly Gly Lys Leu Asn Ile Met
            35                  40                  45

Thr Lys Asp Gly Phe Thr Phe Asp Leu Gly Pro Ser Ile Leu Thr Met
        50                  55                  60

Pro His Ile Phe Glu Ala Leu Phe Thr Gly Ala Gly Lys Asn Met Ala
65                  70                  75                  80

Asp Tyr Val Gln Ile Gln Lys Val Glu Pro His Trp Arg Asn Phe Phe
                85                  90                  95

Glu Asp Gly Ser Val Ile Asp Leu Cys Glu Asp Ala Glu Thr Gln Arg
            100                 105                 110

Arg Glu Leu Asp Lys Leu Gly Pro Gly Thr Tyr Ala Gln Phe Gln Arg
            115                 120                 125

Phe Leu Asp Tyr Ser Lys Asn Leu Cys Thr Glu Thr Glu Ala Gly Tyr
        130                 135                 140

Phe Ala Lys Gly Leu Asp Gly Phe Trp Asp Leu Leu Lys Phe Tyr Gly
145                 150                 155                 160

Pro Leu Arg Ser Leu Leu Ser Phe Asp Val Phe Arg Ser Met Asp Gln
            165                 170                 175

Gly Val Arg Arg Phe Ile Ser Asp Pro Lys Leu Val Glu Ile Leu Asn
            180                 185                 190

Tyr Phe Ile Lys Tyr Val Gly Ser Ser Pro Tyr Asp Ala Pro Ala Leu
        195                 200                 205

Met Asn Leu Leu Pro Tyr Ile Gln Tyr His Tyr Gly Leu Trp Tyr Val
    210                 215                 220

Lys Gly Gly Met Tyr Gly Met Ala Gln Ala Met Glu Lys Leu Ala Val
225                 230                 235                 240
```

29

```
Glu Leu Gly Val Glu Ile Arg Leu Asp Ala Glu Val Ser Glu Ile Gln
              245                     250                 255

Lys Gln Asp Gly Arg Ala Cys Ala Val Lys Leu Ala Asn Gly Asp Val
              260                     265                 270

Leu Pro Ala Asp Ile Val Val Ser Asn Met Glu Val Ile Pro Ala Met
              275                     280                 285

Glu Lys Leu Leu Arg Ser Pro Ala Ser Glu Leu Lys Lys Met Gln Arg
              290                     295                 300

Phe Glu Pro Ser Cys Ser Gly Leu Val Leu His Leu Gly Val Asp Arg
305                     310                 315                 320

Leu Tyr Pro Gln Leu Ala His His Asn Phe Phe Tyr Ser Asp His Pro
              325                     330                 335

Arg Glu His Phe Asp Ala Val Phe Lys Ser His Arg Leu Ser Asp Asp
              340                     345                 350

Pro Thr Ile Tyr Leu Val Ala Pro Cys Lys Thr Asp Pro Ala Gln Ala
              355                     360                 365

Pro Ala Gly Cys Glu Ile Ile Lys Ile Leu Pro His Ile Pro His Leu
              370                     375                 380

Asp Pro Asp Lys Leu Leu Thr Ala Glu Asp Tyr Ser Ala Leu Arg Glu
385                     390                 395                 400

Arg Val Leu Val Lys Leu Glu Arg Met Gly Leu Thr Asp Leu Arg Gln
              405                     410                 415

His Ile Val Thr Glu Glu Tyr Trp Thr Pro Leu Asp Ile Gln Ala Lys
              420                     425                 430

Tyr Tyr Ser Asn Gln Gly Ser Ile Tyr Gly Val Val Ala Asp Arg Phe
              435                     440                 445

Lys Asn Leu Gly Phe Lys Ala Pro Gln Arg Ser Ser Glu Leu Ser Asn
              450                     455                 460

Leu Tyr Phe Val Gly Gly Ser Val Asn Pro Gly Gly Gly Met Pro Met
465                     470                 475                 480
```

30

Val Thr Leu Ser Gly Gln Leu Val Arg Asp Lys Ile Val Ala Asp Leu
                485   490   495

Gln

<210>   25
<211>   912
<212>   DNA
<213>   Pantoea stewartii

<400>   25
ttgacggtct gcgcaaaaaa acacgttcac cttactggca tttcggctga gcagttgctg   60

gctgatatcg atagccgcct tgatcagtta ctgccggttc agggtgagcg ggattgtgtg   120

ggtgccgcga tgcgtgaagg cacgctggca ccgggcaaac gtattcgtcc gatgctgctg   180

ttattaacag cgcgcgatct tggctgtgcg atcagtcacg ggggattact ggatttagcc   240

tgcgcggttg aaatggtgca tgctgcctcg ctgattctgg atgatatgcc ctgcatggac   300

gatgcgcaga tgcgtcgggg cgtcccacc attcacacgc agtacggtga acatgtggcg   360

attctggcgg cggtcgcttt actcagcaaa gcgtttgggg tgattgccga ggctgaaggt   420

ctgacgccga tagccaaaac tcgcgcggtg tcggagctgt ccactgcgat tggcatgcag   480

ggtctggttc agggccagtt taaggacctc tcggaaggcg ataaaccccg cagcgccgat   540

gccatactgc taaccaatca gtttaaaacc agcacgctgt tttgcgcgtc aacgcaaatg   600

gcgtccattg cggccaacgc gtcctgcgaa gcgcgtgaga acctgcatcg tttctcgctc   660

gatctcggcc aggcctttca gttgcttgac gatcttaccg atggcatgac cgataccggc   720

aaagacatca atcaggatgc aggtaaatca acgctggtca atttattagg ctcaggcgcg   780

gtcgaagaac gcctgcgaca gcatttgcgc ctggccagtg aacacctttc cgcggcatgc   840

caaaacggcc attccaccac ccaactttt attcaggcct ggtttgacaa aaaactcgct   900

gccgtcagtt aa   912

<210>   26
<211>   303
<212>   PRT
<213>   Pantoea stewartii

<400>   26

Leu Thr Val Cys Ala Lys Lys His Val His Leu Thr Gly Ile Ser Ala
1   5   10   15

31

```
Glu Gln Leu Leu Ala Asp Ile Asp Ser Arg Leu Asp Gln Leu Leu Pro
            20                  25                  30

Val Gln Gly Glu Arg Asp Cys Val Gly Ala Ala Met Arg Glu Gly Thr
            35                  40                  45

Leu Ala Pro Gly Lys Arg Ile Arg Pro Met Leu Leu Leu Leu Thr Ala
        50                  55                  60

Arg Asp Leu Gly Cys Ala Ile Ser His Gly Gly Leu Leu Asp Leu Ala
65                  70                  75                  80

Cys Ala Val Glu Met Val His Ala Ala Ser Leu Ile Leu Asp Asp Met
                85                  90                  95

Pro Cys Met Asp Asp Ala Gln Met Arg Arg Gly Arg Pro Thr Ile His
            100                 105                 110

Thr Gln Tyr Gly Glu His Val Ala Ile Leu Ala Ala Val Ala Leu Leu
        115                 120                 125

Ser Lys Ala Phe Gly Val Ile Ala Glu Ala Glu Gly Leu Thr Pro Ile
        130                 135                 140

Ala Lys Thr Arg Ala Val Ser Glu Leu Ser Thr Ala Ile Gly Met Gln
145                 150                 155                 160

Gly Leu Val Gln Gly Gln Phe Lys Asp Leu Ser Glu Gly Asp Lys Pro
                165                 170                 175

Arg Ser Ala Asp Ala Ile Leu Leu Thr Asn Gln Phe Lys Thr Ser Thr
            180                 185                 190

Leu Phe Cys Ala Ser Thr Gln Met Ala Ser Ile Ala Ala Asn Ala Ser
        195                 200                 205

Cys Glu Ala Arg Glu Asn Leu His Arg Phe Ser Leu Asp Leu Gly Gln
    210                 215                 220

Ala Phe Gln Leu Leu Asp Asp Leu Thr Asp Gly Met Thr Asp Thr Gly
225                 230                 235                 240

Lys Asp Ile Asn Gln Asp Ala Gly Lys Ser Thr Leu Val Asn Leu Leu
            245                 250                 255
```

32

```
Gly Ser Gly Ala Val Glu Glu Arg Leu Arg Gln His Leu Arg Leu Ala
        260                 265                 270


Ser Glu His Leu Ser Ala Ala Cys Gln Asn Gly His Ser Thr Thr Gln
        275                 280                 285


Leu Phe Ile Gln Ala Trp Phe Asp Lys Lys Leu Ala Ala Val Ser
        290                 295                 300
```

```
<210>   27
<211>   1296
<212>   DNA
<213>   Pantoea stewartii

<400>   27
atgagccatt ttgcggtgat cgcaccgccc tttttcagcc atgttcgcgc tctgcaaaac    60
cttgctcagg aattagtggc ccgcggtcat cgtgttacgt tttttcagca acatgactgc   120
aaagcgctgg taacgggcag cgatatcgga ttccagaccg tcggactgca aacgcatcct   180
cccggttcct tatcgcacct gctgcacctg ccgcgcacc cactcggacc ctcgatgtta    240
cgactgatca atgaaatggc acgtaccagc gatatgcttt gccgggaact gcccgccgct   300
tttcatgcgt tgcagataga gggcgtgatc gttgatcaaa tggagccggc aggtgcagta   360
gtcgcagaag cgtcaggtct gccgtttgtt tcggtggcct gcgcgctgcc gctcaaccgc   420
gaaccgggtt tgcctctggc ggtgatgcct ttcgagtacg gcaccagcga tgcggctcgg   480
gaacgctata ccaccagcga aaaaatttat gactggctga tgcgacgtca cgatcgtgtg   540
atcgcgcatc atgcatgcag aatgggttta gccccgcgtg aaaaactgca tcattgtttt   600
tctccactgg cacaaatcag ccagttgatc cccgaactgg attttccccg caaagcgctg   660
ccagactgct tcatgcggt tggaccgtta cggcaacccc aggggacgcc ggggtcatca    720
acttcttatt ttccgtcccc ggacaaaccc cgtattttg cctcgctggg caccctgcag    780
ggacatcgtt atggcctgtt caggaccatc gccaaagcct gcgaagaggt ggatgcgcag   840
ttactgttgg cacactgtgg cggcctctca gccacgcagg caggtgaact ggcccggggc   900
ggggacattc aggttgtgga ttttgccgat caatccgcag cactttcaca ggcacagttg   960
acaatcacac atggtgggat gaatacggta ctggacgcta ttgcttcccg cacaccgcta  1020
ctggcgctgc cgctggcatt tgatcaacct ggcgtggcat cacgaattgt ttatcatggc  1080
atcggcaagc gtgcgtctcg gtttactacc agccatgcgc tggcgcggca gattcgatcg  1140
ctgctgacta acaccgatta cccgcagcgt atgacaaaaa ttcaggccgc attgcgtctg  1200
```

33

```
gcaggcggca caccagccgc cgccgatatt gttgaacagg cgatgcggac ctgtcagcca      1260

gtactcagtg ggcaggatta tgcaaccgca ctatga                                1296


<210>   28
<211>   431
<212>   PRT
<213>   Pantoea stewartii

<400>   28

Met Ser His Phe Ala Val Ile Ala Pro Pro Phe Phe Ser His Val Arg
1               5               10              15


Ala Leu Gln Asn Leu Ala Gln Glu Leu Val Ala Arg Gly His Arg Val
            20              25              30


Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp
        35              40              45


Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu
    50              55              60


Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu
65              70              75              80


Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu
                85              90              95


Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp
            100             105             110


Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro
        115             120             125


Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu
    130             135             140


Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg
145             150             155             160


Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg
            165             170             175


His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro
            180             185             190
```

```
Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln
        195             200             205

Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe
        210             215             220

His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser
225             230             235             240

Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu
            245             250             255

Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys
            260             265             270

Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly
        275             280             285

Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln
        290             295             300

Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu
305             310             315             320

Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser
            325             330             335

Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val
            340             345             350

Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe
            355             360             365

Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn
        370             375             380

Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu
385             390             395             400

Ala Gly Gly Thr Pro Ala Ala Ala Asp Ile Val Glu Gln Ala Met Arg
            405             410             415

Thr Cys Gln Pro Val Leu Ser Gly Gln Asp Tyr Ala Thr Ala Leu
            420             425             430
```

35

<210> 29
<211> 1149
<212> DNA
<213> Pantoea stewartii

<400> 29

```
atgcaaccgc actatgatct cattctggtc ggtgccggtc tggctaatgg ccttatcgcg    60

ctccggcttc agcaacagca tccggatatg cggatcttgc ttattgaggc gggtcctgag   120

gcgggaggga accatacctg gtcctttcac gaagaggatt taacgctgaa tcagcatcgc   180

tggatagcgc cgcttgtggt ccatcactgg cccgactacc aggttcgttt cccccaacgc   240

cgtcgccatg tgaacagtgg ctactactgc gtgacctccc ggcatttcgc cgggatactc   300

cggcaacagt ttggacaaca tttatggctg cataccgcgg tttcagccgt tcatgctgaa   360

tcggtccagt tagcggatgg ccggattatt catgccagta cagtgatcga cggacggggt   420

tacacgcctg attctgcact acgcgtagga ttccaggcat ttatcggtca ggagtggcaa   480

ctgagcgcgc cgcatggttt atcgtcaccg attatcatgg atgcgacggt cgatcagcaa   540

aatggctacc gctttgttta taccctgccg ctttccgcaa ccgcactgct gatcgaagac   600

acacactaca ttgacaaggc taatcttcag gccgaacggg cgcgtcagaa cattcgcgat   660

tatgctgcgc gacagggttg gccgttacag acgttgctgc gggaagaaca gggtgcattg   720

cccattacgt taacgggcga taatcgtcag ttttggcaac agcaaccgca gcctgtagc    780

ggattacgcg ccgggctgtt tcatccgaca accggctact ccctaccgct cgcggtggcg   840

ctggccgatc gtctcagcgc gctggatgtg tttacctctt cctctgttca ccagacgatt   900

gctcactttg cccagcaacg ttggcagcaa caggggtttt ccgcatgct gaatcgcatg    960

ttgtttttag ccggaccggc cgagtcacgc tggcgtgtga tgcagcgttt ctatggctta  1020

cccgaggatt tgattgcccg cttttatgcg ggaaaactca ccgtgaccga tcggctacgc  1080

attctgagcg gcaagccgcc cgttcccgtt ttcgcggcat gcaggcaat tatgacgact   1140

catcgttga                                                          1149
```

<210> 30
<211> 382
<212> PRT
<213> Pantoea stewartii

<400> 30

```
Met Gln Pro His Tyr Asp Leu Ile Leu Val Gly Ala Gly Leu Ala Asn
1               5                   10                  15


Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln His Pro Asp Met Arg Ile
            20                  25                  30
```

36

```
Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser
        35              40              45

Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro
    50              55              60

Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg
65              70              75              80

Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe
            85              90              95

Ala Gly Ile Leu Arg Gln Gln Phe Gly Gln His Leu Trp Leu His Thr
            100             105             110

Ala Val Ser Ala Val His Ala Glu Ser Val Gln Leu Ala Asp Gly Arg
        115             120             125

Ile Ile His Ala Ser Thr Val Ile Asp Gly Arg Gly Tyr Thr Pro Asp
    130             135             140

Ser Ala Leu Arg Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Gln
145             150             155             160

Leu Ser Ala Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr
            165             170             175

Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Thr Leu Pro Leu Ser
        180             185             190

Ala Thr Ala Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Lys Ala Asn
        195             200             205

Leu Gln Ala Glu Arg Ala Arg Gln Asn Ile Arg Asp Tyr Ala Ala Arg
    210             215             220

Gln Gly Trp Pro Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu
225             230             235             240

Pro Ile Thr Leu Thr Gly Asp Asn Arg Gln Phe Trp Gln Gln Gln Pro
            245             250             255

Gln Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly
            260             265             270
```

37

```
Tyr Ser Leu Pro Leu Ala Val Ala Leu Ala Asp Arg Leu Ser Ala Leu
        275             280             285


Asp Val Phe Thr Ser Ser Ser Val His Gln Thr Ile Ala His Phe Ala
        290             295             300


Gln Gln Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met
305             310             315             320


Leu Phe Leu Ala Gly Pro Ala Glu Ser Arg Trp Arg Val Met Gln Arg
                325             330             335


Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys
                340             345             350


Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val
        355             360             365


Pro Val Phe Ala Ala Leu Gln Ala Ile Met Thr Thr His Arg
        370             375             380


<210>   31
<211>   1479
<212>   DNA
<213>   Pantoea stewartii

<400>   31
atgaaaccaa ctacggtaat tggtgcgggc tttggtggcc tggcactggc aattcgttta        60

caggccgcag gtattcctgt tttgctgctt gagcagcgcg acaagccggg tggccgggct       120

tatgtttatc aggagcaggg ctttactttt gatgcaggcc ctaccgttat caccgatccc       180

agcgcgattg aagaactgtt tgctctggcc ggtaaacagc ttaaggatta cgtcgagctg       240

ttgccggtca cgccgtttta tcgcctgtgc tgggagtccg gcaaggtctt caattacgat       300

aacgaccagg cccagttaga agcgcagata cagcagttta tccgcgcga tgttgcgggt        360

tatcgagcgt ccttgactta ttcgcgtgcc gtattcaatg agggctatct gaagctcggc       420

actgtgcctt ttttatcgtt caaagacatg cttcgggccg cgccccagtt ggcaaagctg       480

caggcatggc gcagcgttta cagtaaagtt gccggctaca ttgaggatga gcatcttcgg       540

caggcgtttt cttttcactc gctcttagtg gggggggaatc cgtttgcaac ctcgtccatt      600

tatacgctga ttcacgcgtt agaacgggaa tggggcgtct ggtttccacg cggtggaacc       660

ggtgcgctgg tcaatggcat gatcaagctg tttcaggatc tgggcggcga agtcgtgctt       720
```

38

```
aacgcccggg tcagtcatat ggaaaccgtt ggggacaaga ttcaggccgt gcagttggaa    780

gacggcagac ggtttgaaac ctgcgcggtg gcgtcgaacg ctgatgttgt acatacctat    840

cgcgatctgc tgtctcagca tcccgcagcc gctaagcagg cgaaaaaact gcaatccaag    900

cgtatgagta actcactgtt tgtactctat tttggtctca accatcatca cgatcaactc    960

gcccatcata ccgtctgttt tgggccacgc taccgtgaac tgattcacga aatttttaac   1020

catgatggtc tggctgagga tttttcgctt tatttacacg caccttgtgt cacggatccg   1080

tcactggcac cggaagggtg cggcagctat tatgtgctgg cgcctgttcc acacttaggc   1140

acggcgaacc tcgactgggc ggtagaagga ccccgactgc gcgatcgtat ttttgactac   1200

cttgagcaac attacatgcc tggcttgcga agccagttgg tgacgcaccg tatgtttacg   1260

ccgttcgatt ccgcgacga gctcaatgcc tggcaaggtt cggccttctc ggttgaacct   1320

attctgaccc agagcgcctg gttccgacca cataaccgcg ataagcacat tgataatctt   1380

tatctggttg gcgcaggcac ccatcctggc gcgggcattc ccggcgtaat cggctcggcg   1440

aaggcgacgg caggcttaat gctggaggac ctgatttga                           1479


<210>    32
<211>    492
<212>    PRT
<213>    Pantoea stewartii

<400>    32

Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
1               5                   10                  15


Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
            20                  25                  30


Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe
        35                  40                  45


Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
    50                  55                  60


Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Asp Tyr Val Glu Leu
65                  70                  75                  80


Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
                85                  90                  95


Phe Asn Tyr Asp Asn Asp Gln Ala Gln Leu Glu Ala Gln Ile Gln Gln
                100                 105                 110
```

39

```
Phe Asn Pro Arg Asp Val Ala Gly Tyr Arg Ala Phe Leu Asp Tyr Ser
        115                 120                 125

Arg Ala Val Phe Asn Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
    130                 135                 140

Leu Ser Phe Lys Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
145                 150                 155                 160

Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Gly Tyr Ile Glu Asp
            165                 170                 175

Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
            180                 185                 190

Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
        195                 200                 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val
    210                 215                 220

Asn Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu
225                 230                 235                 240

Asn Ala Arg Val Ser His Met Glu Thr Val Gly Asp Lys Ile Gln Ala
            245                 250                 255

Val Gln Leu Glu Asp Gly Arg Arg Phe Glu Thr Cys Ala Val Ala Ser
        260                 265                 270

Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro
        275                 280                 285

Ala Ala Ala Lys Gln Ala Lys Lys Leu Gln Ser Lys Arg Met Ser Asn
    290                 295                 300

Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu
305                 310                 315                 320

Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile His
            325                 330                 335

Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
        340                 345                 350
```

40

His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly
        355   360   365

Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
        370   375   380

Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr
385   390   395   400

Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
                405   410   415

Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln
                420   425   430

Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe
        435   440   445

Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly
        450   455   460

Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
465   470   475   480

Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
                485   490

<210>   33
<211>   891
<212>   DNA
<213>   Pantoea stewartii

<400>   33
atggcggttg gctcgaaaag ctttgcgact gcatcgacgc ttttcgacgc caaaacccgt   60

cgcagcgtgc tgatgcttta cgcatggtgc cgccactgcg acgacgtcat tgacgatcaa   120

acactgggct ttcatgccga ccagccctct tcgcagatgc ctgagcagcg cctgcagcag   180

cttgaaatga aaacgcgtca ggcctacgcc ggttcgcaaa tgcacgagcc cgcttttgcc   240

gcgtttcagg aggtcgcgat ggcgcatgat atcgctcccg cctacgcgtt cgaccatctg   300

gaaggttttg ccatggatgt cgcgcgaaacg cgctacctga cactggacga tacgctgcgt   360

tattgctatc acgtcgccgg tgttgtgggc ctgatgatgg cgcaaattat gggcgttcgc   420

gataacgcca cgctcgatcg cgcctgcgat ctcgggctgg ctttccagtt gaccaacatt   480

41

```
gcgcgtgata ttgtcgacga tgctcaggtg ggccgctgtt atctgcctga aagctggctg    540

gaagaggaag gactgacgaa agcgaattat gctgcgccag aaaaccggca ggccttaagc    600

cgtatcgccg ggcgactggt acgggaagcg gaaccctatt acgtatcatc aatggccggt    660

ctggcacaat taccccttacg ctcggcctgg gccatcgcga cagcgaagca ggtgtaccgt    720

aaaattggcg tgaaagttga acaggccggt aagcaggcct gggatcatcg ccagtccacg    780

tccaccgccg aaaaattaac gcttttgctg acggcatccg gtcaggcagt tacttcccgg    840

atgaagacgt atccaccccg tcctgctcat ctctggcagc gcccgatcta g             891
```

<210> 34
<211> 296
<212> PRT
<213> Pantoea stewartii

<400> 34

```
Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Thr Leu Phe Asp
1               5                   10                  15

Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His
                20                  25                  30

Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln
                35                  40                  45

Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys
        50                  55                  60

Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
65                  70                  75                  80

Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
                85                  90                  95

Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr
                100                 105                 110

Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val
            115                 120                 125

Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr
    130                 135                 140

Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile
145                 150                 155                 160
```

42

Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro
                165   170   175

Glu Ser Trp Leu Glu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala
                180   185   190

Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg
                195   200   205

Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu
                210   215   220

Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg
225   230   235   240

Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His
                245   250   255

Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Leu Thr Ala
                260   265   270

Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro
                275   280   285

Ala His Leu Trp Gln Arg Pro Ile
    290   295

<210>   35
<211>   528
<212>   DNA
<213>   Pantoea stewartii

<400>   35
atgttgtgga tttggaatgc cctgatcgtg tttgtcaccg tggtcggcat ggaagtggtt   60

gctgcactgg cacataaata catcatgcac ggctggggtt ggggctggca tctttcacat   120

catgaaccgc gtaaaggcgc atttgaagtt aacgatctct atgccgtggt attcgccatt   180

gtgtcgattg ccctgattta cttcggcagt acaggaatct ggccgctcca gtggattggt   240

gcaggcatga ccgcttatgg tttactgtat tttatggtcc acgacggact ggtacaccag   300

cgctggccgt ccgctacat accgcgcaaa ggctacctga acggttata catggcccac   360

cgtatgcatc atgctgtaag gggaaaagag ggctgcgtgt cctttggttt tctgtacgcg   420

43

```
ccaccgttat ctaaacttca ggcgacgctg agagaaaggc atgcggctag atcgggcgct      480

gccagagatg agcaggacgg ggtggatacg tcttcatccg ggaagtaa                  528
```

<210> 36
<211> 175
<212> PRT
<213> Pantoea stewartii

<400> 36

```
Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly
1               5                  10                  15


Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
                20                  25                  30


Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
                35                  40                  45


Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
        50                  55                  60


Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
65                  70                  75                  80


Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
                85                  90                  95


Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
                100                 105                 110


Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
                115                 120                 125


Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
        130                 135                 140


Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
145                 150                 155                 160


Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
                165                 170                 175
```

<210> 37
<211> 1599
<212> DNA
<213> Rhodococcus erythropolis AN12

<400> 37

```
gtgagcgcat ttctcgacgc cgtcgtcgtc ggttccggac acaacgcgct cgtttcggcc    60

gcgtatctcg cacgtgaggg ttggtcggtc gaggttctcg agaaggacac ggttctcggc   120

ggtgccgtct cgaccgtcga gcgatttccc ggatacaagg tggaccgggg gtcgtctgcg   180

cacctcatga tccgacacag tggcatcatc gaggaactcg gactcggcgc gcacggcctt   240

cgctacatcg actgtgaccc gtgggcgttc gctccgcccg ccctggcac cgacgggccg    300

ggcatcgtgt ttcatcgcga cctcgatgca acctgccagt ccatcgaacg agcttgcggg   360

acaaaggacg ccgacgcgta ccggcggttc gtcgcggtct ggtcggagcg cagccgacac   420

gtgatgaagg cattttccac accgcccacc ggatcgaacc tgatcggtgc gttcggagga   480

ctggccacag cgcgcggcaa cagcgaactg tcgcggcagt cctcgcgcc gggcgacgca    540

ctgctggacg agtatttcga cagtgaggca ctcaaggcag cgttggcgtg gttcggcgcc   600

cagtccgggc ctccgatgtc ggaaccggga accgctccga tggtcggctt cgcggccctc   660

atgcacgtcc tgccgcccgg gcgagcagtc ggagggagcg cgcactgag tgctgcgttg    720

gcatcccgga tggctgtcga cggcgccacc gtcgcgctcg gtgacggcgt gacgtcgatc   780

cgccggaact cgaatcactg gaccgtcaca accgagagcg gtcgagaagt tcacgctcgc   840

aaggtaatcg cgggttgcca catcctcacg acactcgatc tcctgggcaa cggaggcttc   900

gaccgaacca cgctcgatca ctggcggcgg aagatcaggg tcggccccgg catcggcgct   960

gtattgcgac tggcgacatc tgcgctcccg tcctaccgcg gcgacgccac gacacgggaa  1020

agtacctcgg gattgcaatt actcgtttcc gatcgcgccc acttgcgcac tgcacacggc  1080

gcagcactgg cagggg aact gcctcctcgc cctgcggttc tcggaatgag tttcagcgga  1140

atcgatccca cgatcgcccc ggccgggcgg catcaggtga cactgtggtc gcagtggcag  1200

ccgtatcgtc tcagcggaca tcgcgattgg gcgtcggtcg ccgaggccga ggccgaccgg  1260

atcgtcggcg agatggaggc ttttgcaccc ggattcaccg attccgtcct cgaccgcttc  1320

attcaaactc cccgcgacat cgagtcggaa ttggggatga tcggcggaaa tgtcatgcac  1380

gtcgagatgt cactcgatca gatgatgttg tggcgaccgc ttcccgaact gtccggccat  1440

cgcgttccgg gagcagacgg gttgtatctg accggagcct cgacgcatcc cggtggtggt  1500

gtgtccggag ccagtggtcg cagtgccgct cgaatcgcac tgtccgacag ccgccggggt  1560

aaagcgagtc agtggatgcg tcgttcgagc aggtcgtga                         1599
```

<210> 38
<211> 532

<212> PRT
<213> Rhodococcus erythropolis AN12

<400> 38

Met Ser Ala Phe Leu Asp Ala Val Val Val Gly Ser Gly His Asn Ala
1   5   10   15

Leu Val Ser Ala Ala Tyr Leu Ala Arg Glu Gly Trp Ser Val Glu Val
                20   25   30

Leu Glu Lys Asp Thr Val Leu Gly Gly Ala Val Ser Thr Val Glu Arg
            35   40   45

Phe Pro Gly Tyr Lys Val Asp Arg Gly Ser Ser Ala His Leu Met Ile
        50   55   60

Arg His Ser Gly Ile Ile Glu Glu Leu Gly Leu Gly Ala His Gly Leu
65   70   75   80

Arg Tyr Ile Asp Cys Asp Pro Trp Ala Phe Ala Pro Pro Ala Pro Gly
                85   90   95

Thr Asp Gly Pro Gly Ile Val Phe His Arg Asp Leu Asp Ala Thr Cys
            100   105   110

Gln Ser Ile Glu Arg Ala Cys Gly Thr Lys Asp Ala Asp Ala Tyr Arg
            115   120   125

Arg Phe Val Ala Val Trp Ser Glu Arg Ser Arg His Val Met Lys Ala
    130   135   140

Phe Ser Thr Pro Pro Thr Gly Ser Asn Leu Ile Gly Ala Phe Gly Gly
145   150   155   160

Leu Ala Thr Ala Arg Gly Asn Ser Glu Leu Ser Arg Gln Phe Leu Ala
                165   170   175

Pro Gly Asp Ala Leu Leu Asp Glu Tyr Phe Asp Ser Glu Ala Leu Lys
            180   185   190

Ala Ala Leu Ala Trp Phe Gly Ala Gln Ser Gly Pro Pro Met Ser Glu
            195   200   205

Pro Gly Thr Ala Pro Met Val Gly Phe Ala Ala Leu Met His Val Leu
    210   215   220

46

```
Pro Pro Gly Arg Ala Val Gly Gly Ser Gly Ala Leu Ser Ala Ala Leu
225                 230             235                 240

Ala Ser Arg Met Ala Val Asp Gly Ala Thr Val Ala Leu Gly Asp Gly
                245             250                 255

Val Thr Ser Ile Arg Arg Asn Ser Asn His Trp Thr Val Thr Thr Glu
                260             265                 270

Ser Gly Arg Glu Val His Ala Arg Lys Val Ile Ala Gly Cys His Ile
        275             280                 285

Leu Thr Thr Leu Asp Leu Leu Gly Asn Gly Gly Phe Asp Arg Thr Thr
    290             295                 300

Leu Asp His Trp Arg Arg Lys Ile Arg Val Gly Pro Gly Ile Gly Ala
305             310                 315                 320

Val Leu Arg Leu Ala Thr Ser Ala Leu Pro Ser Tyr Arg Gly Asp Ala
                325             330                 335

Thr Thr Arg Glu Ser Thr Ser Gly Leu Gln Leu Leu Val Ser Asp Arg
            340             345                 350

Ala His Leu Arg Thr Ala His Gly Ala Ala Leu Ala Gly Glu Leu Pro
        355             360                 365

Pro Arg Pro Ala Val Leu Gly Met Ser Phe Ser Gly Ile Asp Pro Thr
    370             375                 380

Ile Ala Pro Ala Gly Arg His Gln Val Thr Leu Trp Ser Gln Trp Gln
385             390                 395                 400

Pro Tyr Arg Leu Ser Gly His Arg Asp Trp Ala Ser Val Ala Glu Ala
                405             410                 415

Glu Ala Asp Arg Ile Val Gly Glu Met Glu Ala Phe Ala Pro Gly Phe
            420             425                 430

Thr Asp Ser Val Leu Asp Arg Phe Ile Gln Thr Pro Arg Asp Ile Glu
            435             440                 445

Ser Glu Leu Gly Met Ile Gly Gly Asn Val Met His Val Glu Met Ser
    450             455                 460
```

47

```
Leu Asp Gln Met Met Leu Trp Arg Pro Leu Pro Glu Leu Ser Gly His
465                 470             475             480


Arg Val Pro Gly Ala Asp Gly Leu Tyr Leu Thr Gly Ala Ser Thr His
            485                 490             495


Pro Gly Gly Gly Val Ser Gly Ala Ser Gly Arg Ser Ala Ala Arg Ile
            500             ·505             510


Ala Leu Ser Asp Ser Arg Arg Gly Lys Ala Ser Gln Trp Met Arg Arg
            515             520             525


Ser Ser Arg Ser
    530
```

```
<210>   39
<211>   30
<212>   DNA
<213>   Methylomonas 16a

<400>   39
ccgagtactg aagcgggttt ttgcagggag                                          30


<210>   40
<211>   25
<212>   DNA
<213>   Methylomonas 16a

<400>   40
gggctagctg ctccgattgt tacag                                               25


<210>   41
<211>   38
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer, derived from Rhodococcus erythropolis AN12

<400>   41
agcagctagc ggaggaataa accatgagcg catttctc                                 38


<210>   42
<211>   26
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer, derived from Rhodococcus erythropolis AN12
```

```
<400>  42
gactagtcac gacctgctcg aacgac                                    26


<210>  43
<211>  25
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  43
atgacggtct gcgcaaaaaa acacg                                     25


<210>  44
<211>  28
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  44
gagaaattat gttgtggatt tggaatgc                                  28


<210>  45
<211>  19
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  45
gagtttgatc ctggctcag                                            19


<210>  46
<211>  16
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  46
taccttgtta cgactt                                               16


<210>  47
<211>  17
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer
```

```
<220>
<221>  misc_feature
<222>  (11)..(11)
<223>  Y = C or T


<220>
<221>  misc_feature
<222>  (12)..(12)
<223>  M = A or C


<400>  47
gtgccagcag ymgcggt                                                      17


<210>  48
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  48
atgagcgcat ttctcgacgc c                                                 21


<210>  49
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  49
tcacgacctg ctcgaacgac                                                   20


<210>  50
<211>  50
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  50
gagaattggc tgaaaaacca aataaataac aaaatttagc gagtaaatgg                  50


<210>  51
<211>  50
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer
```

50

```
<400>  51
ttcaattgac aggggggctc gttctgattt agagttgctg ccagcttttt                    50


<210>  52
<211>  50
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  52
gggttgtcca gatgttggtg agcggtcctt ataactataa ctgtaacaat                    50


<210>  53
<211>  50
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  53
ttaatggtct tgccatgaga tgtgctccga ttgttacagt tatagttata                    50


<210>  54
<211>  50
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  54
cccccctgtca attgaaagcc cgccatttac tcgctaaatt ttgttattta                   50


<210>  55
<211>  22
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  55
aaggatccgc gtattcgtac tc                                                   22


<210>  56
<211>  40
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer
```

<400> 56
ctggatccga tctagaaata ggctcgagtt gtcgttcagg   40

<210> 57
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 57
aaggatccta ctcgagctga catcagtgct   30

<210> 58
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 58
gctctagatg caaccagaat cg   22

<210> 59
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 59
tggctcgaga gtaaaacact caag   24

<210> 60
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 60
tagctcgagt cacgcttgc   19